

25 Apr 2007

Alignment Results

EXHIBIT A

Alignment: Global Protein alignment against reference molecule
 Parameters: Scoring matrix: BLOSUM 62

Reference molecule: SEQIDNO:2, Region 1-788

Number of sequences to align: 3

Settings: Similarity significance value cutoff: >= 60%



Summary of Percent Matches:

Reference:	SEQIDNO:2	1 -	788	(788 aa)	--
Sequence 2:	SEQIDNO:11	1 -	788	(788 aa)	97%
Sequence 3:	SEQIDNO:32	1 -	788	(788 aa)	99%

SEQIDNO:2	1	MNKNNTKLSTRALPSFIDYFNGIYGATGIKDIMNMIFKTDGGNLTLDEILKNQQLNE
SEQIDNO:11	1D.....D
SEQIDNO:32	1	..M.....NA.....
SEQIDNO:2	61	ISGLDGVNGSLNDLIAQGNLNTLSKEILKIANEQNQVLNDVNNKLD AINTMLHIYLPK
SEQIDNO:11	61RV.....
SEQIDNO:32	61
SEQIDNO:2	121	ITSMLSDVMKQNYALS LQIEYLSKQLQEISDKLDIINVNVLINSTLTEITPAYQRIKYVN
SEQIDNO:11	121
SEQIDNO:32	121
SEQIDNO:2	181	EKFEELTFATETTLKVKKDSSPADILDELTELAKSVTKNDVDGFEFYLNTHDVMVG
SEQIDNO:11	181SS.....G.....
SEQIDNO:32	181
SEQIDNO:2	241	NNLFGRSALKTASELIAKENVKTS GSEVGNVYNFLIVLTALQAKAFLTLTTCRKLLGLAG
SEQIDNO:11	241T.....D
SEQIDNO:32	241D
SEQIDNO:2	301	IDYTSIMNEHLNKEKEEFVRNIP TLSNTFSNPYAKVKGSEDAKMIVEAKPGHALVGF
SEQIDNO:11	301I.....
SEQIDNO:32	301
SEQIDNO:2	361	EMSND SITVLKVYEAKLKQNYQVDKDSLSEVIYGD TDKLFCPDQSEQIYYTNNIVFPNEY
SEQIDNO:11	361	..I.....M.....I.....
SEQIDNO:32	361
SEQIDNO:2	421	VITKIDFTKKMKTLRYEVTANFYD SSTGEIDLNKKKVESSEAEYRTLSANDDGVYMP LGV
SEQIDNO:11	421
SEQIDNO:32	421
SEQIDNO:2	481	ISFTFLTPINGFGLQADENSRLIT LTCKSYLRELLLATDLSNKETKLIVPPSGFISNIVE
SEQIDNO:11	481
SEQIDNO:32	481
SEQIDNO:2	541	NGSIEEDNLEPWKANNKNAYVDHT GG VNGTKALYVHKDGGFSQFIGDKLKP KTEYVIQYT
SEQIDNO:11	541I.....
SEQIDNO:32	541
SEQIDNO:2	601	VKGKPSIHLK DENTGYIHYEDTNNNLKDYQTITKRFTTG TDLKGVYLILKSQNGDEAWGD
SEQIDNO:11	601E.....N.....
SEQIDNO:32	601
SEQIDNO:2	661	KFTILEIKPAEDLLSPELINPNSWITTPGASISGNKLFINLGTNGTFRQSLSLNSYSTYS
SEQIDNO:11	661
SEQIDNO:32	661
SEQIDNO:2	721	ISFTASGPFNVTVRNSRXVLFERSNLMSSTSHISGTFKTESNNTGLYVELSRRSGGGGHI
SEQIDNO:11	721G.....
SEQIDNO:32	721E.....

SEQIDNO:2	781 SFENVSIK
SEQIDNO:11	781
SEQIDNO:32	781

A “.” means the amino acids are identical at that position.

26 Apr 2007

Alignment Results

EXHIBIT B

Alignment: Global Protein alignment against reference molecule

Parameters: Scoring matrix: BLOSUM 62

Reference molecule: SEQIDNO:2, Region 1-788

Number of sequences to align: 2

Settings: Similarity significance value cutoff: >= 60%

Summary of Percent Matches:

Reference:	SEQIDNO:2	1 -	788	(788 aa)	--
Sequence 2:	86BB1(c)	1 -	789	(789 aa)	90%

SEQIDNO:2	1	MNKNNTKLSTRALPSFIDYFNGIYG	FATGIKDIMNMI	FKTDTGGNLT	LDEILKNQ	QLLNE
86BB1(c)	1
SEQIDNO:2	61	ISGKLDGVNGSLNDLIAQGNLN	TELSKEILKIANEQNQVLNDV	NNKLDAINTML	HIYLPK	
86BB1(c)	61
SEQIDNO:2	121	ITSMLSDVMKQNYALSLQIEYLS	KQLQEISDKLDI	INVNVLIN	STLTEITPAY	QRIKYVN
86BB1(c)	121
SEQIDNO:2	181	EKFEELTFATETTLKVKKDSS	PADILDELTELAKSVTKND	VDGFEFYLN	T	FHDVMVG
86BB1(c)	181G.....S.....Q.....
SEQIDNO:2	241	NNLFGRSALKTASELIAKEN	VKTSGSEVGNVYNFLIV	L	TALQAKAFL	TLTTCRKLLGLAG
86BB1(c)	241D
SEQIDNO:2	301	IDYTSIMNEHLNKEKEEF	RVN	ILPTLSNTFS	NPYAKVKG	SDEDAKMIVEAKPGHALVGF
86BB1(c)	301Y.....
SEQIDNO:2	361	EMSND	SITVLKVYEAKLKQNYQ	V	KDSLSEVIY	GD
86BB1(c)	361L.....
SEQIDNO:2	421	VITKIDFTKKMKTLRYE	TANFYDSSTGEIDL	NKKKVESSEAEY	RTLSAN	DDGVYMP
86BB1(c)	421
SEQIDNO:2	481	IS	ETFLTPINGFGLQADENS	RLITLTCKSYLRE	LLATDLSN	KETKLIVPPSGFISNIVE
86BB1(c)	481G.....L.....
SEQIDNO:2	541	NGSIEEDNLEPWKANN	KNAYVDHTGGVNGTK	ALYVHKDGG	FSQFIGDKL	KPKTEYVIQYT
86BB1(c)	541
SEQIDNO:2	601	VKGKPSIHLKDENTGYI	HYEDTNNNLKDYQTIT	KRFTTG	TDLKG	VYLILKSQNGDEAWGD
86BB1(c)	601
SEQIDNO:2	661	KFTILEIKPAEDLLSPE	LINPNSWITTPGASIS	GNKLFINLGT	NGTFROSLS	LSNSTYS
86BB1(c)	661	N.T....S.S.K.....T.N.TS.GSTH....T.TLYQ.GR.ILK.N.Q.D.F...R
SEQIDNO:2	721	ISFTASGPFNVTVRNS	RXLVLFERSNLMSST	SHISGTFKTES	NN	TGLYVELSRRSG--GGG
86BB1(c)	721	VY.SV..DA..RI....E....K-RY..GAKDV.EM.T.KFEKDNF.T...QGNNLY..P
SEQIDNO:2	779	HISFENVSIK				
86BB1(c)	780	IVH.ND....				

A "." means the amino acids are identical at that position.